

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2002, 21:30:39 : Search time 1944.37 Seconds
(Without alignments)
1246.212 Million cell updates/sec

Title: US-09-719-017A-2

Perfect score: 1793
Sequence: 1 gattcccggtgacacatca.....caatactcaatgcccgcg 1793

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrc:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	139	7.8	888	12 AQ329770	nbxb0045P
C 2	137.4	7.7	1073	12 AF114216	AF114216
C 3	104.4	5.8	544	12 AQ989631	AF020197
C 4	104	5.8	655	12 AQ990982	AF020183
C 5	100.6	5.6	1101	12 AF029514	AF029514
C 6	99	5.5	622	12 AQ329769	AF029769
C 7	83.6	4.7	580	12 AQ160684	nbxb0006L
C 8	82.2	4.6	409	9 AW711275	AW711275
C 9	76.4	4.3	417	9 AW713376	g8c04ne.f
C 10	74.2	4.1	417	9 AW710819	g8c04ne.f
C 11	73	4.1	330	9 BE092318	IL2-BT073
C 12	72.2	4.0	694	9 AM948136	RC0-MT001
C 13	72.2	4.0	707	9 AM948129	RC0-MT001
C 14	72.2	4.0	708	9 AM948148	RC0-MT001
C 15	72.2	4.0	730	9 AM948130	RC0-MT001
C 16	72.2	4.0	738	9 AM948138	RC0-MT001
C 17	71.8	4.0	633	9 AM948152	RC0-MT001

18	69	3.8	643	9 AM948147	AM948147 RC0-MT001
19	66.8	3.7	359	9 AW710710	AW710710 esf03ne.f
20	53.4	3.0	348	9 AW708603	AW708603 c9e12ne.f
21	53.4	3.0	360	9 AW714224	AW714224 h6g09ne.f
C 22	52.8	2.9	434	9 AF408416	AF408416
C 23	52	2.9	532	10 BG278308	BG278308 a3d02np.f
C 24	51.6	2.9	918	12 AF114188	AF114188
C 25	49.2	2.7	730	12 BH390360	BH390360 AG-ND-166
C 26	48.2	2.7	477	10 BE600147	BE600147 P11_79_H0
C 27	47.8	2.7	412	9 A1329382	A1329382 b4a1one.f
C 28	47.6	2.7	507	10 BF484942	BF484942 WHE2333.D
C 29	46.6	2.6	419	10 BF072824	BF072824 NCSP7C3F3
C 30	46.4	2.6	925	12 CNS0091P	AL053013 Drosophila
C 31	46	2.6	417	10 BF473461	BF473461 WHE0924.F
C 32	45.4	2.5	259	10 BM373215	BM373215 E8ma04_SO
C 33	45.4	2.5	294	10 BM43910	BM43910 E8em09_SO
C 34	45.4	2.5	295	10 BM098909	BM098909 EBP105_5Q
C 35	45.4	2.5	462	12 AQ016380	AQ016380 CIT-HSP-2
C 36	45.4	2.5	498	9 AV942445	AV942445 AV942445
C 37	45.4	2.5	577	9 AV945848	AV945848 AV945848
C 38	45.4	2.5	633	9 AV944572	AV944572 AV944572
C 39	45.4	2.5	719	12 AG010512	AG010512 Homo sapi
C 40	45.2	2.5	539	10 BE604694	BE604694 WHE1413-1
C 41	44.8	2.5	688	10 BG912542	BG912542 602806648
C 42	44.6	2.5	516	10 BE434941	BE434941 EST7406019
C 43	44.6	2.5	517	10 B1269359	B1269359 NF008A071
C 44	44.6	2.5	520	10 B1269270	B1269270 NF0056121
C 45	44.6	2.5	564	10 BE460888	BE460888 EST412307

ALIGNMENTS

RESULT 1
AQ329770/c 888 bp DNA linear GSS 08-JAN-1999
LOCUS nbxb0045P09r CUGI Rice BAC Library Oryza sativa genomic clone
DEFINITION nbxb0045P09r. DNA sequence.

ACCESSION AQ329770.1 GI:4121620
VERSION AQ329770
KEYWORDS GSS.

SOURCE Oryza sativa.
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing Ra
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

FEATURES
Source Email: twing@clemson.edu
Seq primer: GGAAACACTGACCATG
Class: BAC ends
High quality sequence start: 13
High quality sequence stop: 225.
Location/Qualifiers
1..888
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nbxb0045P09r"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
/lab_host="E. coli DH10b"
/note="Vector: pBel06Acl1; Site 1: HindIII; Site 2:
HindIII; Rice is one of two most popular grains in the


```
library"
/dev_stage="primary phase variant"
/notes="Genomic DNA from strain W14
kb) and then cloned into M13 Janus
BASE COUNT      129 a      108 c      123 g      183 t      1 others
ORIGIN
```

Query Match	5.8%	Score 104.4	DB 12	Length 544
Best Local Similarity	75.9%	Pred. No. 1.1e-18		
Matches 129, Conservative	0	Mismatches 41	Indels 0	Gaps 0

Qy	1268	g	a	t	c	g	a	c	c	t	g	c	a	g	c	a	t	y	c	a	a	g	c	t	t	y	g	t	c	c	a	c	t	y	a	c	c	c	a	t	y	c	c	g	a	a	c	t	c	a	a	a	g	t	1327
Db	47	G	A	A	T	A	T	G	C	T	G	G	G	G	C	A	T	A	G	C	G	C	G	T	G	T	T	C	C	A	C	C	T	G	A	C	C	C	A	T	G	C	C	A	C	T	C	A	G	A	G	T	106		

Qy 1328 gaacacgcctgtagcgccgtagtctgggggtctcccatgcaagataggaactgcga 138
|||||
Db 107 GAACGCCCTAGCGCCGATGCTAGTGTGGGGTCTCCCATGTGAGAGTAGACACTGCCA 166

Qy 1388 ygcatacaataaacaagcgtcagtcgaagaactyggcccttcgttt 1437
 ||| ||||| | ||| ||| ||| |||
 Db 167 GGCTTAATACAGTGAACCCCTCAGCGTAAGCTGGGGTTTTGCGTT 216

RESULT	4
AQ990982	

LOCUS	655 bp	DNA	linear	GSS 14-AUG
DEFINITION	RfC01832	Photorhabdus luminescens strain W14 M13 library		
	Photorhabdus luminescens genomic clone PLG01832, DNA sequence			

VERSION AQ990982.1 GI:9649576

SOURCE ORGANISM	Photorhabdus luminescens. Photorhabdus luminescens
100	100
98	98
96	96
94	94
92	92
90	90
88	88
86	86
84	84
82	82
80	80
78	78
76	76
74	74
72	72
70	70
68	68
66	66
64	64
62	62
60	60
58	58
56	56
54	54
52	52
50	50
48	48
46	46
44	44
42	42
40	40
38	38
36	36
34	34
32	32
30	30
28	28
26	26
24	24
22	22
20	20
18	18
16	16
14	14
12	12
10	10
8	8
6	6
4	4
2	2
0	0

REFERENCE 1 (bases 1 to 655)

AUTHORS
 ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium *Photobacterium luminescens* W14: potential implications for virulence
JOURNAL
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry

University Of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsarfr@bath.ac.uk
This is one of 2,132 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see Ifrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES	location/qualifiers
source	1. .655

```

/organism="Photorhabdus luminescens"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01832"
/clone_1b="Photorhabdus luminescens strain W14 M13
library"

```

```

,
/dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into the pTZ19 vector."

```

	kd)	and	then	cloned	into	M13	vectors.
BASE COUNT	173	a	160	c	170	g	151 t
ORIGIN							1 others

Query match	5.88; Score 104; DB 12; Length 655;
-------------	-------------------------------------

Best Local Similarity	72.8%;	Pred. No.	1.5e-18;
Matches	134;	Conservative	0;
		Mismatches	50;
		Indels	0;
		Gaps	0;

Oy 1268 gaagtcgaacctgcaaggcatgcgaactgttggtccaccctcacaacccaatggcgaaactcaagaagt 132
 ||| |
 ||| |
Db 56 GAATATGCTGGCGGGCGATTACGCCGGGTGCCACCAGCCCAATGC CGAACTCAGCAGT 115

Qy 1328 gaaacgcgtagcgcgagtagtqtagtqggtctcccatqcgagtagtgaactgcc 1387
 |||||
 Db 116 GAACGCCGTAGCGCCGATGCTGCTGGGCTCTCCCATGTGAGAGTAGACACTGCCA 175

Qy 1388 ggcacaaataaaaagcgaagctcagtcgcaagaagclyggcccttgcgtttatcttgtt 144
||| ||||| | | | | | | | | | | | | | | |
Db 176 GGCCTTTAAATACAGTGGCAACCCTCACCAGTAAGCTGGGGGTTTTTGCGTTTAAAGCATR 235

QY	1448	tgtc	1451
Db	236	TCTC	239

RESULT 5
AF029514

LOCUS	1101 bp	DNA	linear	GSS 29-AUG
DEFINITION	AF029514	<i>Salmonella typhimurium</i> LT2, lambda DASH II <i>Salmonella typhimurium</i> genomic clone 715-17, DNA sequence.		

VERSION AF029514.1 GI:2571044

KEYWORDS GSS.
SOURCE *Salmonella typhimurium*.

ORGANISM
Salmonella typhimurium
Bacteria; proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.

REFERENCE	AUTHORS	TITLE
1 (cases 1 to 1101)	Wong, R.M.-Y., Wong, K.K., Benson, N.R. and McClelland, M.	Sample sequencing of a <i>Salmonella typhimurium</i> LT2 lambda library:

comparison to the *Escherichia coli* K12 genome
FEMS Microbiol. Lett. 173 (2), 411-423 (1999)

COMMENT	CONTACT	DATE	TIME	LOCATION	STATUS
99243/5/	McClelland M				

Molecular Biology
Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego, CA 92121, USA
Email: mcclellandellfsci.sdsu.edu
Class: shotgun.

```

Class: shotgun.
FEATURES
  Location/Qualifiers
    1..1101
    source

```

```
/organism="Salmonella typhimurium"
/strain="LT2"
/ab_wref="ttwccv603"
```

```

/uu_xref= laxun:ovz
/clone="715-T7"
/clone_lib="Salmoella turbimurium IT2" lambda DASH IT"

```

```

/chr10:1113- salmonella cf/philadelphia 123/, lambda 123
/note="Vector: Lambda DASH II; sequenced using Li-Cor
sequencer"

```

BASE COUNT	289 a	248 c	319 g	232 t	13 others
ORIGIN					

Query Match	5.68;	Score 100.6;	DB 12;	Length 1101;
Best Local Similarity	86.08;	Pred. No. 1.8e-17;		

Matches	123;	Conservative	0;	Mismatches	19;	Indels	1;	Gaps	1;
---------	------	--------------	----	------------	-----	--------	----	------	----

[illegible]

00 1327 taaatcccgatgcccgaatgatgatgagatctcccatgcacaaatgagaaatgcc 1386

Db 758 TGAACGCCGTAGCCGATGTAGTGTGGGGCTT-CCCATCGAGAGTAGGGAATGCC 816

QY 1387 aggcataataaacgaaagc 1409

Db 817 AGGCATCAATTAGAAGTATGCC 839

```

RESULT 6
LOCUS AO329769 622 bp DNA linear GSS 08-JAN-1999
DEFINITION nbxb0045f09f CUGI Rice BAC Library Oryza sativa genomic clone
ACCESSION AO329769
VERSION AO329769
KEYWORDS AO329769.1 GI:4121619
SOURCE GSS.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 622)
AUTHORS Wang, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACCTCCTATAGG
Class: BAC ends
High quality sequence stop: 423.

FEATURES
SOURCE
location/qualifiers
1..622
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nbxb0045f09f"
/clone_11b="CUGI Rice BAC Library"
/tissue_type="leaf"
/lab_host="E. coli DH10B"
/note="Vector: pGelBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Aruruganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,864 clones with an average insert size
of 128.5 kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."

BASE COUNT 112 a 200 c 190 g 119 t 1 others
ORIGIN
Query Match 5.5%; Score 99; DB 12; Length 622;
Best Local Similarity 54.9%; Pred. NO. 4e-17;
Matches 195; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

693 tcgcgtacaggaacagccatcgcgtcgcacgcgcaggtgaacatgctgcctcgca 752
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 TGCCTCTACAGAGGCAAGCTTTCGCCGCTCGCTCCGAGCTCAACAATGCCCTCAGCCG 61

753 atcattcgttgtaagaccagtgcttaccatcgcgcgcgcagcagtgctgcacccagag 812
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
62 gtctacgcgcgcgcgagagcaatgcttgcgtagatgcgcgccttcgggggtgtttctcgcaa 121

```

Oy	813	acccgagcaccgctcgggaagtagtgaacaacaagccctccctcgctgaagtgagggcgcgcc	872
Db	122	ATGATCCAGCGTGAATGTGGATACCCGAGGAGGACGCCGACTTCTGTCGCCGGGGGCGCGCC	181
Oy	873	agttccatgatctttgcgcgcgagcagcgcacatctgctccctcaactcgtccacacagatgcc	932
Db	182	TATGGAGATCTTATGGTCCCGATGGCGCGCGCGATGGGAAACCAATCGCACCTGAGGAG	241
Oy	933	gaagggcctgatcatctgcgcgactctgaacatgtgaagaattgccttcgcgcaagggcgatcaac	992
Db	242	GAGGCCCTCGATGTCGCCGACATCGATCTGTGATGATGTCCTGACGCAAGACCGCGCA	301
Oy	993	gaacctgtggtgcacactctccaacaccgaggtccaccgctctggtacctggagaccgtg	1047
Db	302	GACCCGACCCGACATTTATGCGCGACACAGCGTCCGACGCCCTTTTTCAMCCCGG	356

RESULT	7	
LOCUS	AO160684	580 bp DNA linear GSS: 09-SEP-1998
DEFINITION	mgxB0006L04r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxB0006L04r, DNA sequence.	
ACCESSION	AO160684	
VERSION	AO160684.1	GI:3557673
KEYWORDS	GSS.	
SOURCE	Magnaporthe grisea.	
ORGANISM	Magnaporthe grisea	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.	
AUTHORS	1 (bases 1 to 580) Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wang, R.A. and Dean, R.A.	
TITLE	A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Dean RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634 Tel: 864 656 5737 Fax: 864 656 4293 Email: rdean@clemson.edu Seq primer: GGAAACAGCTATGCACG Class: BAC ends	
FEATURES	High quality sequence stop: 357. Location/Qualifiers	
Source	1..580	
	/organism="Magnaporthe grisea"	
	/strain="70-15"	
	/db_xref="taxon:148305"	
	/clone="mgxB0006L04r"	
	/clone_lib="CUGI Rice Blast BAC Library"	
	/tissue_type="Protoplasts"	
	/lab_host="E. coli DH10B"	
	/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 1300 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."	
BASE COUNT	132 a 176 c 159 g 113 t	
ORIGIN		
Query Match	4.7%;	Score 83.6; DB 12; Length 580;
Best Local Similarity	54.2%;	Pred. No. 1e-12;
Matches 192; Conservative	0; Mismatches 159; Indels 3; Gaps 1;	

Query Match	4.68;	Score 82.2;	DB 9;	Length 409;
Best Local Similarity	51.58;	Pred. No. 2.2e-12;		
Matches 189; Conservative	0;	Mismatches 178;	Indels 0;	Gaps 0;

```

/organism="Neurospora crassa"
/strain="Strain 30-7 (bd, A)"
/db_xref="taxon:5141"
/clone="g8c04ne"
/clone_11b="Neurospora crassa evenng cdna library"
/tissue_type="tissue harvested following 22hr growth in
dark"
/notes="Vector: pBluescript SK-; Site_1: XbaI; Site_2:
EcoRI; SpeI; Bell-Pardersen,D., et al. PNAS 93:13096, 1996
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT
94 a 136 c 103 g 85 t

```

BASE COUNT	ORIGIN
94 a	136 c
103 g	85 t


```
/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone_lib="M70013"  
/dev_stage="Adult"  
/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESEN5 PCR [U.S. Letters Patent application No. 156  
716 - Ludwig Institute for Cancer Research] profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low
```

Query match 4.08; Score 72.2; DB 9; Length 707;

DB	Accession	Gene	Species	Length	Score	DB	Length	Score	DB	Length	Score
Best Local	Similarity	78.9%	Pred. No. 2.1e-09	Mismatches	23	Indels	0	Gaps	0		
Matches	86	Conservative	0	Mismatches	23	Indels	0	Gaps	0		
OY	1289	agcttgagtcaccactgacccatgacgaatcagaagtgaagccgtagccgcatg	1348								
Db	563	AGCATTGGACCACTGTATCCATCCCGACACAGCAACATGATGATCCGATG	504								
OY	1349	tatgttgaggtctcccatgacgaagttaggaacgcgcgcatacaat	1397								
Db	503	TAGTGTGGCGTTTCCCATGTGACGATGATGCTCAAGATTAAATT	455								
RESULT	14										
LOCUS	AM948148/C	708 bp	mRNA	Linear	EST 31-MAY-2000						
DEFINITION	RCO-MT0013-280300-031-e04	MT0013	Homo sapiens	CDNA	mRNA sequence.						
ACCESSION	AM948148										
KEYWORDS	AM948148.1	GI:8125922									
VERSION	EST.										
SOURCE	human.										
ORGANISM	Homo sapiens										
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.										
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J., and Simpson, A. J.										
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags										
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)	3491-3496	(2000)							
MEDLINE	20202653										
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et2-RCO-MT0013-280300-031-e04&t3=2000-03-28&t4=1) Seq primer: puc 18 forward High quality sequence start: 65 High quality sequence stop: 676 Location/Qualifiers										
FEATURES	source	1..708									
	/organism="Homo sapiens"										
	/db_xref="taxon:9606"										
	/clone_id="MT0013"										
	/dev_stage="Adult"										
	/note="Organ: marrow; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters patent application No. 196 , 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."										
BASE COUNT	164 a	172 c	201 g	171 t							
ORIGIN											
Query Match	4.0%	Score 72.2	DB 9	Length 708							
Best Local Similarity	78.9%	Pred. No. 2.1e-09									
Matches	86	Conservative	0	Mismatches	23	Indels	0	Gaps	0		
OY	1289	agcttgagtcaccactgacccatgacgaatcagaagtgaagccgtagccgcatg	1348								
Db	561	AGCATTGGACCACTGTATCCATCCCGACACAGCAACATGATGATCCGATG	502								

Oy	1349	taagtctggaggtctcccatgacgagtgagggaacgcgcgcgcatcaaat	1397
Db	501	TAGTGTGGGGTTTCCCATGTGAGAGTAGGTGATGCTCAAGATTAAATT	453
RESULT	15		
LOCUS	AM948130/c	730 bp	mRNA
DEFINITION	RCO-MT0013-280300-031-b09 MT0013 Homo sapiens cDNA, mRNA sequence.		EST 31-MAY-2000
ACCESSION	AM948130		
VERSION	AM948130.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 730) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagaï, M. A., da Silva, M. J., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	200202663		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL: (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=4t2-RCO-MT0013-280300-031-b09&t3=2000-03-28&t4=1) Seq primer: puc 18 forward High quality sequence start: 9 High quality sequence stop: 666. Location/Qualifiers 1..730 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MT0013" /dev_stage="Adult" /note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESSES PCR (U.S. Letters Patent application No. 199716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
FEATURES	source		
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Oy	1349	taagtctggaggtctcccatgacgagtgagggaacgcgcgcgcatcaaat	1397
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Search completed: September 17, 2002, 00:35:53
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1
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3